IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Confirmation No.:
Zauderer, M.	Art Unit: To be assigned
Appl. No. To be assigned	Examiner: To be assigned
Filed: Herewith	Atty. Docket: 1821.0010002
For: **Methods of Selecting Polynucleotides Encoding Antigens (as amended herein)**	

Preliminary Amendment

Commissioner for Patents
Washington, D.C. 20231

Sir:

In advance of prosecution, please amend the application as follows. This Amendment is provided in the following format:

(A) A clean version of each replacement paragraph/section/claim along with clear instructions for entry;

(B) Starting on a separate page, appropriate remarks and arguments. 37 C.F.R. § 1.111 and MPEP 714; and

(C) Starting on a separate page, a marked-up version entitled: "Version with markings to show changes made."

It is not believed that extensions of time or fees for net addition of claims are required beyond those that may otherwise be provided for in documents accompanying this paper. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor (including fees for net addition of claims) are hereby authorized to be charged to our Deposit Account No. 19-0036.

Amendments

In the Title

Please cancel the pending title and replace it with the following title:

Methods of Selecting Polynucleotides Encoding Antigens

In the Claims:

Please cancel claims 1-38 without prejudice or disclaimer.

Please add the following new claims:

39. (new) A method for selecting a nucleic acid molecule encoding a target epitope of cytotoxic T-lymphocytes, comprising:

(a) contacting host cells with cytotoxic T-lymphocytes specific for said target epitope under conditions wherein a host cell expressing said target epitope undergoes a lytic event upon contact with said cytotoxic T-lymphocytes; wherein said host cells comprise a library of heterologous nucleic acid molecules, at least one of said heterologous nucleic acid molecules encoding said target epitope, wherein said library is constructed in a vector which expresses said target epitope in said host cells, wherein said host cells express a defined MHC molecule, and wherein said cytotoxic T-lymphocytes are restricted for said MHC molecule; and

(b) recovering those host cells which have undergone a lytic event;

wherein said target epitope is selected from the group consisting of: a target epitope which is differentially expressed in infected cells and a target epitope which is specific for an autoimmune disease.

40. (new) The method of claim 39, wherein said target epitope is differentially expressed in infected cells.

41. (new) The method of claim 40, wherein said infected cells are infected with a pathogen selected from the group consisting of: a virus, a fungus, and a mycobacterium.

42. (new) The method of claim 41, wherein said pathogen is a virus.

43. (new) The method of claim 41, wherein said infected cells are infected with a fungus.

44. (new) The method of claim 41, wherein said infected cells are infected with a mycobacterium.

45. (new) The method of claim 39, further comprising isolating said vector from those host cells which have undergone a lytic event.

46. (new) The method of claim 39, further comprising:

(a) isolating said vector from those host cells which have undergone a lytic event;

(b) transferring said vector to a population of host cells, wherein said vector expresses said target epitope in said host cells, and wherein said host cells express a defined MHC molecule;

(c) contacting said host cells with cytotoxic T-lymphocytes specific for said target epitope and restricted for said MHC molecule, under conditions wherein a host cell expressing said target epitope will undergo a lytic event upon contact with said cytotoxic T-lymphocytes; and

(d) recovering those host cells which have undergone a lytic event.

47. (new) The method of claim 39, wherein said vector is a virus.

48. (new) The method of claim 47, wherein said vector is a virus capable of producing infectious viral particles in eukaryotic cells.

49. (new) The method of claim 48, wherein the naturally-occurring genome of said viral vector is linear, double stranded DNA.

50. (new) The method of claim 48, wherein said viral vector is capable of producing infectious viral particles in mammalian cells.

51. (new) The method of claim 50, wherein the naturally-occurring genome of said viral vector is linear, double-stranded DNA.

52. (new) The method of claim 48, wherein said viral vector is a poxvirus vector.

53. (new) The method of claim 52, wherein said viral vector is a vaccinia virus vector.

54. (new) The method of claim 47, wherein said host cells are permissive for the production of infectious viral particles of said viral vector.

55. (new) The method of claim 52, wherein said viral vector further comprises a transcriptional control signal in operable association with said heterologous nucleic acid molecules, and wherein said transcriptional control signal functions in a poxvirus.

56. (new) The method of claim 55, wherein said transcriptional control signal comprises a promoter.

57. (new) The method of claim 56, wherein said promoter is constitutive.

58. (new) The method of claim 56, wherein said promoter is selected from the group consisting of: a vaccinia virus p7.5 promoter and a synthetic early/late promoter.

59. (new) The method of claim 55, wherein said transcriptional control signal comprises a transcriptional termination signal.

60. (new) The method of claim 55, wherein said vector further comprises a translational control signal associated with said transcriptional control signal.

61. (new) The method of claim 60, wherein said translational control signal comprises a translation initiation codon operably linked to said heterologous nucleic acid molecules.

62. (new) The method of claim 61, wherein said translation initiation codon occurs in one of three reading frames.

63. (new) The method of claim 49, wherein said library is constructed by a method comprising:

(a) cleaving an isolated linear DNA virus genome to produce a first viral fragment and a second viral fragment, wherein said first fragment is nonhomologous with said second fragment;

(b) providing a population of transfer plasmids comprising said heterologous nucleic acid molecules flanked by a 5' flanking region and a 3' flanking region, wherein said 5' flanking region is homologous to said first viral fragment and said 3' flanking region is homologous to said second viral fragment; and wherein said transfer plasmids are

capable of homologous recombination with said first and second viral fragments such that a viable virus genome is formed;

(c) introducing said transfer plasmids and said first and second viral fragments into a host cell under conditions wherein a transfer plasmid and said viral fragments undergo *in vivo* homologous recombination, thereby producing a viable modified virus genome comprising a heterologous nucleic acid molecule; and

(d) recovering said modified virus genome.

64. (new) The method of claim 63, wherein said virus genome comprises a first recognition site for a first restriction endonuclease and a second recognition site for a second restriction endonuclease; and wherein said first and second viral fragments are produced by digesting said viral genome with said first restriction endonuclease and said second restriction endonuclease, and isolating said first and second viral fragments.

65. (new) The method of claim 64, wherein said first and second recognition sites are physically arranged in said genome such that the region extending between said first and second viral fragments is not essential for virus infectivity.

66. (new) The method of claim 63, wherein said modified virus genome is packaged in an infectious viral particle.

67. (new) The method of claim 51, wherein said library is constructed by a method comprising:

(a) cleaving an isolated linear DNA virus genome to produce a first viral fragment and a second viral fragment, wherein said first fragment is nonhomologous with said second fragment;

(b) providing a population of transfer plasmids comprising said heterologous nucleic acid molecules flanked by a 5' flanking region and a 3' flanking region, wherein said 5' flanking region is homologous to said first viral fragment and said 3' flanking region is homologous to said second viral fragment; and wherein said transfer plasmids are capable of homologous recombination with said first and second viral fragments such that a viable virus genome is formed;

(c) introducing said transfer plasmids and said first and second viral fragments into a host cell under conditions wherein a transfer plasmid and said viral fragments undergo *in vivo* homologous recombination, thereby producing a viable modified virus genome comprising a heterologous nucleic acid molecule; and

(d) recovering said modified virus genome.

68. (new) The method of claim 67, wherein said virus genome comprises a first recognition site for a first restriction endonuclease and a second recognition site for a second restriction endonuclease; and wherein said first and second viral fragments are produced by digesting said viral genome with said first restriction endonuclease and said second restriction endonuclease, and isolating said first and second viral fragments.

69. (new) The method of claim 68, wherein said first and second recognition sites are physically arranged in said genome such that the region extending between said first and second viral fragments is not essential for virus infectivity.

70. (new) The method of claim 67, wherein said isolated virus genome is a poxvirus genome.

71. (new) The method of claim 70, wherein said poxvirus genome is a vaccinia virus genome.

72. (new) The method of claim 70, wherein said transfer plasmids and said first and second viral fragments are introduced into a host cell comprising a helper virus, wherein said host cell is non-permissive for the production of infectious virus particles of said helper virus.

73. (new) The method of claim 72, wherein said helper virus is an avipoxvirus.

74. (new) The method of claim 73, wherein said helper virus is a fowlpox virus.

75. (new) The method of claim 68, wherein said first and second restriction enzyme recognition sites are situated in a thymidine kinase gene.

76. (new) The method of claim 70, wherein said first and second restriction enzyme recognition sites are situated in a vaccinia virus HindIII J fragment.

77. (new) The method of claim 76, wherein said first and second restriction enzyme recognition sites are situated in a vaccinia virus thymidine kinase gene.

78. (new) The method of claim 76, wherein said first restriction enzyme is NotI, and wherein said first restriction enzyme recognition site is GCGGCCGC.

79. (new) The method of claim 76, wherein said second restriction enzyme site is ApaI, and wherein said second restriction enzyme recognition site is GGGCCC.

80. (new) The method of claim 71, wherein said isolated virus genome is a v7.5/tk virus genome.

81. (new) The method of claim 71, wherein said isolated virus genome is a vEL/tk virus genome.

82. (new) The method of claim 70, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus thymidine kinase gene.

83. (new) The method of claim 82, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus HindIII J fragment.

84. (new) The method of claim 82, wherein said transfer plasmids comprise heterologous nucleic acid molecules ligated into a plasmid selected from the group consisting of:

(a) p7.5/ATG0/tk,

(b) p7.5/ATG1/tk,

(c) p7.5/ATG2/tk, and

(d) p7.5/ATG3/tk.

85. (new) The method of claim 39, wherein said host cells are a monolayer, and wherein those host cells which have undergone a lytic event are released from said monolayer.

86. (new) The method of claim 39, wherein said MHC molecule is a class I MHC molecule.

87. (new) The method of claim 46, wherein said host cells are a monolayer, and wherein those host cells which have undergone a lytic event are released from said monolayer.

88. (new) The method of claim 46, wherein said MHC molecule is a class I MHC molecule.

Remarks

Reconsideration of this Application is respectfully requested.

Upon entry of the foregoing amendment, claims 39-88 are pending in the application, with claim 39 being the independent claim. Claims 1-38 are cancelled without prejudice to or disclaimer of the subject matter therein. New claims 39-88 are added. Support for claims 39-88 can be found throughout the specification and claims as originally filed. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Applicants believe that the application is now in condition for examination. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Prompt and favorable consideration of this Amendment is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

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Date: January 3, 2002

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Version with markings to show changes made

In the Title:

Methods of Selecting Polynucleotides Encoding [T Cells Specific for Target] Antigens [and Methods and Vaccines Based Thereon]

In the Claims:

Claims 1-38 have been cancelled.

New claims 39-88 have been added.